

#6
PCT09
26.02

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/868,987

DATE: 10/29/2001

TIME: 13:48:41

Input Set : A:\pto_vsk.txt

Output Set: N:\CRF3\10292001\I868987.raw

P.5

4 <110> APPLICANT: Aventis Pasteur Limited
 6 <120> TITLE OF INVENTION: Chlamydia antigens and corresponding DNA fragments and uses thereof
 8 <130> FILE REFERENCE: 77813-5
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/868,987
 C--> 11 <141> CURRENT FILING DATE: 2001-10-01
 13 <150> PRIOR APPLICATION NUMBER: 60/113,280
 14 <151> PRIOR FILING DATE: 1998-12-23
 16 <150> PRIOR APPLICATION NUMBER: 60/113,281
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 31 <150> PRIOR APPLICATION NUMBER: 60/113,385
 32 <151> PRIOR FILING DATE: 1998-12-23
 34 <150> PRIOR APPLICATION NUMBER: 60/114,050
 35 <151> PRIOR FILING DATE: 1998-12-28
 37 <150> PRIOR APPLICATION NUMBER: 60/114,056
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 40 <150> PRIOR APPLICATION NUMBER: 60/114,057
 41 <151> PRIOR FILING DATE: 1998-12-28
 43 <150> PRIOR APPLICATION NUMBER: 60/114,058
 44 <151> PRIOR FILING DATE: 1998-12-28
 46 <150> PRIOR APPLICATION NUMBER: 60/114,059
 47 <151> PRIOR FILING DATE: 1998-12-28
 49 <150> PRIOR APPLICATION NUMBER: 60/114,061
 50 <151> PRIOR FILING DATE: 1998-12-28
 52 <160> NUMBER OF SEQ ID NOS: 26
 54 <170> SOFTWARE: PatentIn Ver. 2.0
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 58 <212> TYPE: DNA
 59 <213> ORGANISM: Chlamydia pneumoniae
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 62 <221> NAME/KEY: CDS
 63 <222> LOCATION: (101)..(1756)
 65 <400> SEQUENCE: 1
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 68 aaaccgtgga tggcgtatgg ctgtagtgtat tgacggttat atg gtc agc agc cct 115
 69 Met Val Ser Ser Pro
 70 1 5
 72 att tta aac gtc cca ttg aaa aat cat gcc agt gtc tca ggg aaa ttt 163
 73 Ile Leu Asn Val Pro Leu Lys Asn His Ala Ser Val Ser Gly Lys Phe

ENTERED

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80	atg	tct	ttt	gtt	ccc	gag	gtt
81	Met	Ser	Phe	Val	Pro	Glu	Val
82			40			45	
84	ctt	ggg	aaa	aaa	caa	tgt	aca
85	Leu	Gly	Lys	Lys	Gln	Cys	Thr
86			55			60	
88	ttg	gca	atg	ctt	att	gtt	ttg
89	Leu	Ala	Met	Leu	Ile	Val	Leu
90	70					75	
92	gtc	atc	gct	tcg	gga	gct	gtt
93	Val	Ile	Ala	Ser	Gly	Ala	Val
94						90	
96	gct	cta	cag	tat	ttg	gat	gcg
97	Ala	Leu	Gln	Tyr	Leu	Asp	Ala
98						105	
100	att	gtt	ctt	gct	atg	ggg	atg
101	Ile	Val	Leu	Ala	Met	Gly	Met
102						120	
104	gaa	aga	atc	cga	gag	gaa	ttt
105	Glu	Arg	Ile	Arg	Glu	Glu	Phe
106						135	
108	gta	gaa	aaa	gga	tat	acc	aag
109	Val	Glu	Lys	Gly	Tyr	Thr	Lys
110	150					155	
112	ttg	act	aca	gta	ttg	gcc	tca
113	Leu	Thr	Thr	Val	Leu	Ala	Ser
114						170	
116	cct	att	aaa	ggg	ttt	gct	ttg
117	Pro	Ile	Lys	Gly	Phe	Ala	Leu
118						185	
120	atg	ttt	acg	gct	ctt	ttc	atg
121	Met	Phe	Thr	Ala	Leu	Phe	Met
122						200	
124	aat	aag	acc	caa	cat	aca	cag
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126						215	
128	ata	aag	cat	gat	ttc	ttg	aga
129	Ile	Lys	His	Asp	Phe	Leu	Arg
130	230					235	
132	gga	agt	gtt	ttt	ctt	tta	ggt
133	Gly	Ser	Val	Phe	Leu	Leu	Gly
134						250	
136	aat	tcc	gtt	ttg	gga	atg	gat
137	Asn	Ser	Val	Leu	Gly	Met	Asp
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140	aat	cca	aaa	gag	cat	ggc	atc	agc	gat	gtt	gct	caa	atg	cgt	ggc	aaa	979
141	Asn	Pro	Lys	Glu	His	Gly	Ile	Ser	Asp	Val	Ala	Gln	Met	Arg	Gly	Lys	
142			280					285					290				
144	gtt	gtg	cat	aaa	cta	cag	gaa	gct	ggt	ctt	tct	tct	aga	gac	ttc	cgt	1027
145	Val	Val	His	Lys	Leu	Gln	Glu	Ala	Gly	Leu	Ser	Ser	Arg	Asp	Phe	Arg	
146		295					300					305					
148	att	caa	aca	ttt	gga	tct	tca	gaa	aag	atc	aaa	atc	tat	ttt	agt	gat	1075
149	Ile	Gln	Thr	Phe	Gly	Ser	Ser	Glu	Lys	Ile	Lys	Ile	Tyr	Phe	Ser	Asp	
150	310					315					320					325	
152	aaa	gct	tta	agc	tat	act	aag	cag	ata	cga	gcc	tct	ctc	cta	aaa	tta	1123
153	Lys	Ala	Leu	Ser	Tyr	Thr	Lys	Gln	Ile	Arg	Ala	Ser	Leu	Leu	Lys	Leu	
154			330						335					340			
156	acg	atc	atg	agc	tgg	cgt	tat	tgt	ggg	att	gtt	gtc	aga	aac	agg	cct	1171
157	Thr	Ile	Met	Ser	Trp	Arg	Tyr	Cys	Gly	Ile	Val	Val	Arg	Asn	Arg	Pro	
158			345						350					355			
160	aga	ttt	ctc	tac	gga	aac	tct	aaa	cga	aac	gca	aaa	ttt	tgg	tca	aag	1219
161	Arg	Phe	Leu	Tyr	Gly	Asn	Ser	Lys	Arg	Asn	Ala	Lys	Phe	Trp	Ser	Lys	
162			360						365					370			
164	gta	agc	agc	aaa	cta	tcg	aag	aaa	atg	cgt	tat	cag	gcg	acc	atc	ggg	1267
165	Val	Ser	Ser	Lys	Leu	Ser	Lys	Lys	Met	Arg	Tyr	Gln	Ala	Thr	Ile	Gly	
166			375						380					385			
168	ctt	tta	gga	gct	ttg	gca	atc	atc	ttg	ctc	tat	gtg	agt	ttg	cgc	ttt	1315
169	Leu	Leu	Gly	Ala	Leu	Ala	Ile	Ile	Leu	Leu	Tyr	Val	Ser	Leu	Arg	Phe	
170	390					395					400					405	
172	gaa	tgg	caa	tat	gct	ttc	agt	gcc	gta	tgc	gct	tta	att	cat	gac	ctt	1363
173	Glu	Trp	Gln	Tyr	Ala	Phe	Ser	Ala	Val	Cys	Ala	Leu	Ile	His	Asp	Leu	
174				410						415					420		
176	ttg	gct	acc	tgt	gca	gtc	ttg	ttt	ata	gca	cat	ttc	ttt	ttg	aag	aaa	1411
177	Leu	Ala	Thr	Cys	Ala	Val	Leu	Phe	Ile	Ala	His	Phe	Phe	Leu	Lys	Lys	
178			425						430					435			
180	att	caa	ata	gat	ttg	caa	gcc	att	ggt	gct	tta	atg	act	gta	ttg	ggg	1459
181	Ile	Gln	Ile	Asp	Leu	Gln	Ala	Ile	Gly	Ala	Leu	Met	Thr	Val	Leu	Gly	
182			440						445					450			
184	tat	tca	tta	aac	aat	act	ttg	atc	att	ttt	gat	cgt	att	cgt	gaa	gat	1507
185	Tyr	Ser	Leu	Asn	Asn	Thr	Leu	Ile	Ile	Phe	Asp	Arg	Ile	Arg	Glu	Asp	
186			455						460					465			
188	cgc	caa	gcg	aac	ctg	ttt	acc	cct	atg	cat	gtt	tta	gtt	aat	gat	gcc	1555
189	Arg	Gln	Ala	Asn	Leu	Phe	Thr	Pro	Met	His	Val	Leu	Val	Asn	Asp	Ala	
190	470					475					480					485	
192	ctt	caa	aag	acg	ttc	agc	cgc	acg	gta	atg	aca	aca	gct	aca	act	cta	1603
193	Leu	Gln	Lys	Thr	Phe	Ser	Arg	Thr	Val	Met	Thr	Thr	Ala	Thr	Thr	Leu	
194			490								495					500	
196	tca	gtt	ttg	tta	atg	ctt	ttg	ttt	ata	ggc	ggc	tcc	tct	gtc	ttt	aat	1651
197	Ser	Val	Leu	Leu	Met	Leu	Leu	Phe	Ile	Gly	Gly	Ser	Ser	Val	Phe	Asn	
198			505						510					515			
201	ttt	gca	ttt	att	atg	acc	ata	ggg	att	ctt	cta	gga	act	tta	tcg	tct	1699
202	Phe	Ala	Phe	Ile	Met	Thr	Ile	Gly	Ile	Leu	Leu	Gly	Thr	Leu	Ser	Ser	
203			520						525					530			
205	ctt	tat	att	gca	cca	cct	ctg	ttg	ttg	ttt	atg	gtc	cgt	aaa	gaa	aat	1747

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206 Leu Tyr Ile Ala Pro Pro Leu Leu Leu Phe Met Val Arg Lys Glu Asn
207      535                      540                      545
209 cgc tca aaa taagtaccgt taaacttaat ctaacgtgta gcaatataaa      1796
210 Arg Ser Lys
211 550
213 aatctccttt gggacttttag tcccaaaggc ccctgtggta ttaaatttat gacaaattca 1856
215 gataatgc      1864
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221 <212> TYPE: DNA
222 <213> ORGANISM: Chlamydia pneumoniae
224 <220> FEATURE:
225 <221> NAME/KEY: CDS
226 <222> LOCATION: (101)..(688)
228 <400> SEQUENCE: 2
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231 gtgtaacctg cttcttttagg aactacacta ggagaacggt atg tca tca aat cta 115
232                               Met Ser Ser Asn Leu
233                               1           5
235 cat ccc gta gga gga aca gga aca gga gca gct gct cct gag tct gtg 163
236 His Pro Val Gly Gly Thr Gly Thr Gly Ala Ala Ala Pro Glu Ser Val
237      10                      15                      20
239 cta aac ata gta gag gaa ata gca gca tcg ggg agt gtc acc gct ggt 211
240 Leu Asn Ile Val Glu Glu Ile Ala Ala Ser Gly Ser Val Thr Ala Gly
241      25                      30                      35
243 cta caa gca att acg tcc agt cca gga atg gtg aat cta ctc ata gga 259
244 Leu Gln Ala Ile Thr Ser Ser Pro Gly Met Val Asn Leu Leu Ile Gly
245      40                      45                      50
247 tgg gca aag aca aaa ttt att caa cct ata cgt gaa tca aag ctc ttt 307
248 Trp Ala Lys Thr Lys Phe Ile Gln Pro Ile Arg Glu Ser Lys Leu Phe
249      55                      60                      65
251 caa tcc aga gct tgc caa att acc ctg ctc gtt tta gga att ctt ttg 355
252 Gln Ser Arg Ala Cys Gln Ile Thr Leu Leu Val Leu Gly Ile Leu Leu
253 70                      75                      80                      85
255 gtt gtt gct gga tta gca tgt atg ttt atc ttc cat agc cag tta ggg 403
256 Val Val Ala Gly Leu Ala Cys Met Phe Ile Phe His Ser Gln Leu Gly
257      90                      95                      100
259 gca aat gca ttt tgg ttg att att cct gct gcc ata gga ttg att aag 451
260 Ala Asn Ala Phe Trp Leu Ile Ile Pro Ala Ala Ile Gly Leu Ile Lys
261      105                      110                      115
263 tta cta gtt aca tca tta tgt ttt gat gaa gct tgt aca tct gaa aaa 499
264 Leu Leu Val Thr Ser Leu Cys Phe Asp Glu Ala Cys Thr Ser Glu Lys
265      120                      125                      130
267 ctc atg gtt ttc caa aaa tgg gca ggt gtt tta gaa gat cag ctc gat 547
268 Leu Met Val Phe Gln Lys Trp Ala Gly Val Leu Glu Asp Gln Leu Asp
269      135                      140                      145
271 gat ggg atc ctt aat aac tca aat aag att ttt ggc cat gtg aaa aca 595
272 Asp Gly Ile Leu Asn Asn Ser Asn Lys Ile Phe Gly His Val Lys Thr
273 150                      155                      160                      165

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275 gaa gga aat acc tct agg gct act acc cca gta ctt aat gat ggc cgc 643
276 Glu Gly Asn Thr Ser Arg Ala Thr Thr Pro Val Leu Asn Asp Gly Arg
277          170          175          180
279 gga act cct gta ctt tca cct tta gta agt aaa ata gct cgc gtt 688
280 Gly Thr Pro Val Leu Ser Pro Leu Val Ser Lys Ile Ala Arg Val
281          185          190          195
283 tagacgttca tctcacaagc atcctagaac ttgggatgct actttccacg tacgagatca 748
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289 <211> LENGTH: 950
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291 <213> ORGANISM: Chlamydia pneumoniae
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294 <221> NAME/KEY: CDS
295 <222> LOCATION: (101)..(835)
297 <400> SEQUENCE: 3
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301                               Met Thr Ile Arg Ile
302                               1           5
304 ctt gct gaa ggc cta gct ttc cgt tac gga agc aag gga ccg aat atc 163
305 Leu Ala Glu Gly Leu Ala Phe Arg Tyr Gly Ser Lys Gly Pro Asn Ile
306          10          15          20
308 att cat gat gtt tct ttc tct gtc tat gat ggc gac ttt ata gga atc 211
309 Ile His Asp Val Ser Phe Ser Val Tyr Asp Gly Asp Phe Ile Gly Ile
310          25          30          35
312 ata gga cca aac gga ggg ggg aaa agc acc tta acg atg tta att ttg 259
313 Ile Gly Pro Asn Gly Gly Gly Lys Ser Thr Leu Thr Met Leu Ile Leu
314          40          45          50
316 ggc ttg ctt act cct aca ttc gga tcc ttg aag act ttc cct tcg cat 307
317 Gly Leu Leu Thr Pro Thr Phe Gly Ser Leu Lys Thr Phe Pro Ser His
318          55          60          65
320 tcc gcg ggg aaa caa acc cat tcc atg atc ggt tgg gtt ccc caa cat 355
321 Ser Ala Gly Lys Gln Thr His Ser Met Ile Gly Trp Val Pro Gln His
322 70          75          80          85
324 ttc tct tat gat cct tgt ttt cct atc tca gta aaa gat gtt gtc ctc 403
325 Phe Ser Tyr Asp Pro Cys Phe Pro Ile Ser Val Lys Asp Val Val Leu
326          90          95          100
328 tca gga aga ttg tct caa ctc tcc tgg cat gga aaa tat aaa aag aaa 451
329 Ser Gly Arg Leu Ser Gln Leu Ser Trp His Gly Lys Tyr Lys Lys Lys
330          105          110          115
332 gat ttt gaa gct gta gat cac gct ttg gat ctt gtt gga ctt tct gac 499
333 Asp Phe Glu Ala Val Asp His Ala Leu Asp Leu Val Gly Leu Ser Asp
334          120          125          130
336 acc acc acc act gct ttc gcc cat ctc tca gga gga caa atc cag cgt 547
337 Thr Thr Thr Thr Ala Phe Ala His Leu Ser Gly Gly Gln Ile Gln Arg
338          135          140          145
340 gta ctt ctg gca aga gcc tta gcc tcc tac cct gaa att tta att ctt 595
341 Val Leu Leu Ala Arg Ala Leu Ala Ser Tyr Pro Glu Ile Leu Ile Leu

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Use of n and/or Xaa has been detected in the Sequence Listing.

Review the Sequence Listing to insure a corresponding
 explanation is presented in the <220> to <223> fields of
 each sequence using n or Xaa.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/868,987

DATE: 10/29/2001

TIME: 13:48:42

Input Set : A:\pto_vsk.txt

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L:10 M:270 C: Current Application Number differs, Replaced Current Application Number

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:959 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7

L:963 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7